

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 15:49:26 ; Search time 140.11 Seconds
(without alignments)
85.357 Million cell updates/sec

Title: US-09-331-631A-3
Perfect score: 3532
Sequence: 1 MAINTSNLCSLFLFLSLFL.....SSRSTKQOQPLVSLIDVGF 666

Scoring table:
BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1145	32.4	566	1	US-07-955-905A-2 Sequence 2, App11
2	1145	32.4	566	1	US-07-955-905A-22 Sequence 22, App1
3	1069	30.3	587	1	US-07-955-905A-23 Sequence 23, App1
4	853.5	24.2	605	1	US-07-955-905A-24 Sequence 24, App1
5	832.5	23.6	571	1	US-07-955-905A-25 Sequence 25, App1
6	704.5	19.9	410	1	US-07-955-905A-26 Sequence 26, App1
7	557	15.8	421	1	US-07-955-905A-27 Sequence 27, App1
8	226	6.4	1898	1	US-08-056-200-94 Sequence 94, App1
9	226	6.4	1898	2	US-08-800-644-94 Sequence 94, App1
10	218.5	6.2	1162	2	US-08-728-323A-2 Sequence 2, App11
11	146	4.1	303	1	US-08-109-391A-2 Sequence 2, App11
12	146	4.1	303	1	US-08-459-019A-2 Sequence 2, App11
13	146	4.1	303	2	US-08-460-428A-2 Sequence 2, App11
14	146	4.1	303	3	US-08-458-860A-2 Sequence 2, App11
15	140.5	4.0	683	5	5210183-3 Patent No. 5210183
16	139.5	3.9	788	2	US-08-918-914-4 Sequence 4, App11
17	137.5	3.9	558	1	US-08-285-440-6 Sequence 6, App11
18	137.5	3.9	558	1	US-08-630-349-6 Sequence 6, App11
19	136	3.9	186	2	US-08-557-309B-43 Sequence 43, App1
20	136	3.9	186	2	US-08-834-306-43 Sequence 43, App1
21	135.5	3.8	1805	1	US-07-853-913-2 Sequence 2, App11
22	134.5	3.8	614	4	PCT-US95-03236-21 Sequence 21, App1
23	133.5	3.8	2101	1	US-08-466-390-4 Sequence 4, App11
24	133.5	3.8	2101	1	US-08-470-950-4 Sequence 4, App11
25	133.5	3.8	2101	1	US-08-467-781-4 Sequence 4, App11
26	133.5	3.8	2101	1	US-08-195-487-4 Sequence 4, App11
27	133.5	3.8	2101	2	US-08-483-924-4 Sequence 4, App11
28	133.5	3.8	2101	4	PCT-US93-06160-4 Sequence 4, App11

29	133	3.8	1354	3	US-08-685-871-2 Sequence 2, App11
30	130	3.7	432	2	US-08-933-750C-47 Sequence 47, App1
31	130	3.7	432	2	US-09-234-613-47 Sequence 47, App1
32	126.5	3.6	514	2	US-08-960-022-14 Sequence 14, App1
33	123	3.5	3248	1	US-08-353-700-1 Sequence 1, App11
34	123	3.5	3248	4	PCT-US95-16216-1 Sequence 1, App11
35	122	3.5	816	1	US-08-190-802A-54 Sequence 54, App1
36	119.5	3.4	290	2	US-08-903-801-1 Sequence 1, App11
37	119.5	3.4	344	5	5210183-2 Patent No. 5210183
38	119	3.4	905	2	US-08-574-959A-9 Sequence 9, App11
39	119	3.4	1135	2	US-08-574-959A-7 Sequence 7, App11
40	118	3.3	714	2	US-08-990-114-3 Sequence 3, App11
41	117.5	3.3	930	3	US-09-283-763-2 Sequence 2, App11
42	117	3.3	1227	2	US-08-760-075A-18 Sequence 18, App1
43	116.5	3.3	1001	3	US-09-060-410-2 Sequence 2, App11
44	115	3.3	712	2	US-08-468-576B-17 Sequence 17, App1
45	115	3.3	712	2	US-08-468-579B-17 Sequence 17, App1

ALIGNMENTS

```
RESULT 1
US-07-955-905A-2
; Sequence 2, Application US/07955905A
; Patent No. 5770433
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: RECOMBINANT 47 AND 31 KD COCOA PROTEINS AND
; NUMBER OF INVENTION: PRECURSOR
; NUMBER OF SEQUENCES: 28
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/955, 905A
; FILING DATE: 21-JAN-1993
; CLASSIFICATION: 435
; INFORMATION FOR SEQ. ID NO.: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 566 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-955-905A-2
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Query Match 32.4%; Score 1145; DB 1; Length 566;
Best Local Similarity 41.1%; Pred. No. 1.6e-97;
Matches 237; Conservative 107; Mismatches 175; Indels 50; Gaps 13;

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QY 109 ICEEEFYR---QRPQOYEEQCEKRCQHETPRHMQTCQRCERRERKQOKRY 165
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 22 LCGSVASVGRKQYERPRQOYEEQCEKRCSEATEEEQCEQRCR-----EX 70

QY 166 EEOQREDEEKEEYERMKEDDKRPPQOYREYDCRRCEQOE--PRQYOCORCREQORH 223
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 71 KEORQOQEEEL-----ORQYOCQCGRCQOQOQOQOQOQOQOQOQOQOQOQO 116

QY 224 GRGDLINPORGSGRYEEGEKQSDNPYYFDE-RSLSTFRTEEGHISYLENFYGRSKL 282
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 117 ER-GEHENVHNHKNKNSSEEGQRRNPYYFPRKRSFORFRDEGNFKILOFAENSP 175

QY 283 LRLKRYLVLEANPNAYLPYTHLDAALILVTGGRGALKMIRHNRRESYNIEGQVIR 342
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 176 LKQINDYRLAMEFANPTFLPHHCDAEAIYFVTKGKGTITFVTHNKESYNQRTVVS 235

QY 343 IPGCTGYVILNRNNRNLHAKFLQITSPGCKKEFPAGGQNDPEYLSYFSKELIENAL 402
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 236 VPAGSTVYVVSQDNQKLTITAVLALFVNSBQKTELEFPAGNNKPESYGAFTYELTVF 295
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[illegible]

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RESULT      2
US-07-955-905A-22
; Sequence 22: Application US/07955905A
; Patent No. 5770433
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: RECOMBINANT 47 AND 31 KD COCOA PROTEINS AND
; TITLE OF INVENTION: PRECURSOR
; NUMBER OF SEQUENCES: 28
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/955, 905A
; FILING DATE: 21-JAN-1993
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 566 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Theobroma cacao
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..566
; OTHER INFORMATION: /note= "67 kD Precursor Protein"
; US-07-955-905A-22

```

Query Match	32.48;	Score 1145;	DB 1;	Length 566;
Best Local Similarity	41.18;	Pred. NO. 1.6e-97;		
Matches 237;	Conservative 107;	Mismatches 175;	Indels 58;	Gaps 13;

Qy	109	ICEEEEEKNR---	ORDPOXOECOEORSHETPRHNOTOQOCSERYEKKKKQKRY	165
		: : : : : :	: : : : : :	
Db	22	LCSGVSAQGRXRYEEDPPOQYECORRCESEATERTEROEBCRSCER	-----EY	70
		: : : : : :	: : : : : :	
Qy	166	EEQOREDEKYEEMKKEEDNKRDEFOQREYEDCRRRCOE-	PROQYOCORRCOEOROH	223
		: : : : : :	: : : : : :	
Db	71	KEQORQOEEL-----	QRYOCQGRCEQDQOGREQOQCRKCEYQKEQ	116
		: : : : : :	: : : : : :	
Qy	224	GRGGDLNPPQRCGGRYEEGEEKOSDNPPYFDE-	RSLSREPRTEEGHISYLENFYGSKL	262
		: : : : : :	: : : : : :	
Db	117	ER-GEHENYHHKKNRSEEGQORNNPPYPRKRRSFOTRDERDEGNFKILQRAENSP	175	
		: : : : : :	: : : : : :	
Qy	283	LRLAKNRVLLVLEENPNPAFVPTPLDADAILLVYGGGALKMHNRDNRESYNLECGVIR	342	
		: : : : : :	: : : : : :	
Db	176	LKGINDRVLAFFENPNPFIPLPHSCDAEATFYVNGKCTITFEVHEKESLNVOGRGVIS	235	
		: : : : : :	: : : : : :	

[illegible]

```

RESULT      3
US-07-955-905A-23
; Sequence 23 Application US/07955905A
; Patent No. 5770433
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: RECOMBINANT 47 AND 31 KD COCOA PROTEINS AND
; TITLE OF INVENTION: PRECURSOR
; NUMBER OF SEQUENCES: 28
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/955,905A
; FILING DATE: 21-JAN-1993
; CLASSIFICATION: 435
; INFORMATION FOR SEQ. ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 587 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Gossypium hirsutum
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..587
; OTHER INFORMATION: /note= "Vicilin from G. hirsutum"
US-07-955-905A-23

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Query Match	30.3%;	Score 1069;	DB 1;	length 587;
Best Local Similarity	38.1%;	Pred. No. 1.8e-90;		
Matches 228;	Conservative 115;	Mismatches 182;	Indels 74;	Gaps 14;

	Query Match	30.3%;	Score 1069;	DB 1;	Length 587;
	Best Local Similarity	38.1%;	Pred. No. 1.8e-90;		
	Matches 228;	Conservative 115;	Mismatches 182;	Indels 74;	Gaps
OY	76 DDPTDCCOOCRCRQZSGFRQDYCRCK - EICEEETYNQRPPQOYEEOQCRCQ	134			
	: : :	: : :	: : :	:	
Db	35 DDPKRYEDCRRRCFMDTRGQKEQQCEESCSQYGKDQDRHRPDPQRVEECQECR	94			
OY	135 RHETPRHMQTCQRCERRYEKERRKKQKRQEEOQREDEEKYEERMKEEDNKRDPQOREY	194			
	- : - : :	- : - : :	- : - : :	- : - : :	
Db	95 --QOEERQPCQQRQ-----IKRFQQQOO-----SQRF	123			
OY	195 EDCCRRCQEQ--PRQYQOCRCREQORQHGRGDLINPR-----GGSGRYEESEK	246			
	::::: : : :	::: :	::: :	::: :	

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Db      124  QSCQCHQHQDEQRPKQQAQVAECERQYQ-----NPMRRREBEAEDEEETBEEQDE 175
Qy      247  QSDNYIYEDERSLSTRFTTEGHSIVLENFGRSKLLBALKNRYLVLEAPNPAVLPYTH 306
Db      176  QSHNPFHHRSPFSQFRFEEGNGFRVLORFASRRPILRGINEFRLSLLEAPNTEVLPYH 235
Qy      307  LDADAILLVGSRGALKIHHNDNEESVNLCEGDVIRIPAGTFPLIRDNNEIRLHTAKFL 366
Db      236  CDAEKIYIYVNGKGLTFPLTHNKESINNVPGVYVRYPAGSTIYLANQDKKELIAYLVH 295
Qy      367  QTISTPGQYKKEFFPAGGNPEPILYSTEKTELALNTQAEIRLGVGQ-----QOREG 419
Db      296  RPNVNPQGEFEFFPAGSRQPSYLARFSREILBPAPNTRSEQDELDELGHQSHRQOGG 355
Qy      420  VLIASQSOIQLBELTRDSESRHHIIRGGESSRQPYLVFNKRLPYLSKTKQATVEKPEY 479
Db      356  MFRKASQOQLALSOEATSPR---EKSGE--RFAFMILRLTPRYSNQNRFPYACAPREP 409
Qy      480  RQLQMDVSVFLANTQGSMMGPFENFRSTKVVVVAVSGEADVENACPHLSGRHGRRGK 539
Db      410  RQLSDINTVYALQNGSIIIVPHYNSKATFVYLVNNGNGYEVKVSHPLRQSSFEDEE 469
Qy      540  RHEEEDV-----HYEQKARLSKREAIYVPGHPVYVSSGNGENLLLPAGF-----IN 588
Db      470  QOOEOEEOEERRSGQYRKIRLSQSRGDIFFVPANFPVTFVAASQNGNLRMTGFLYNGIN 529
Qy      569  AONNHENTLARENVLDQOTEPQAMETAFAPARKVEBELFNSODESIFFGPRHQOQS 647
Db      530  PDHNRILFVACKINHV-RQWDSQAKELAFGVSSRLVDEIFNNPNQDSFYVS-RQORAS 586

RESULT      4
US-07-955-905A-24
; Sequence 24, Application US/07955905A
; Patent No. 5770433
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: RECOMBINANT 47 AND 31 KD COCOA PROTEINS AND
; TITLE OF INVENTION: PRECURSOR
; NUMBER OF SEQUENCES: 28
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/955,905A
; FILING DATE: 21-JAN-1993
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 605 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..605
; OTHER INFORMATION: /note= "Vicilin from G. max"
US-07-955-905A-24

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Query Match	24.2%	Score 853.5;	DB 1,	Length 605;
Best Local Similarity	31.4%;	Pred No. 1.6e-70;		
Matches 194;	Conservative 143;	Mismatches 211;	Indels 69;	Gaps 15

[illegible][illegible]

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RESULT 5
US-07-955-905A-25
? Sequence 25, Application US/07955905A
? Patent No. 5770433
? GENERAL INFORMATION:
? APPLICANT:
? TITLE OF INVENTION: RECOMBINANT 47 AND 31 KD COCOA PROTEINS AND
? TITLE OF INVENTION: PRECURSOR
? NUMBER OF SEQUENCES: 28
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/07/955,905A
? FILING DATE: 21-JAN-1993
? CLASSIFICATION: 435
? INFORMATION FOR SEQ ID NO: 25:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 571 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? ORIGINAL SOURCE:
? ORGANISM: Pisum sativum
? FEATURE:
? NAME/KEY: Protein
? LOCATION: 1..571
? OTHER INFORMATION: /note="Conviction from P. sativum"
US-07-955-905A-25

```



```

APPLICANT: Frank, Glenn R.
APPLICANT: Grievé, Robert B.
TITLE OF INVENTION: NOVEL PARASITIC HELMINTH
TITLE OF INVENTION: P22U PROTEINS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESS: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: CO
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,428A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-13-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/863-9700
TELEFAX: 303/863-0223
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-460-428A-2

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Query Match 4.1%; Score 146; DB 2; Length 303;
Best Local Similarity 24.6%; Pred. No. 1.6e-05;
Matches 52; Conservative 46; Mismatches 87; Indels 26; Gaps 10;

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```

QY 32 DROEYECRKQ--CMQLETS---GOMRRC--VSQCDKRFEE-----DIDMSKYDNDPP 78
DB 97 DDEDLDECSQGERPCRYLAKTLICVHLKICDGDGSDSDENKADDEVITISINNESI 156
QY 79 QTDCCQCCQRCRCQESGP--RQOQYCORR--CKEICEEBE--EYNRPDPQOQYEQCCQERC 133
DB 157 NTRCDQDQRC--ENGKICIAQIDRCNRKRYDCDDGTDETCFVQALQARGVTVDNA 213
QY 134 QRETEPRHMQTCQRCER-RYEKERKROOKRYEQQREDEEYERMKEDNKRPQOR 192
DB 214 IRDDELPTNTVSMEOKYDYQKEDKERRMOEEEOERLREYEOIQKLOEEREROEOE 273
QY 193 EYEDCRRCEOEPRQOYQCCQRCRCROQROH 223
DB 274 RKQKERERMEQERIRQEYD---EKERQROY 300

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RESULT 14
US-08-458-860A-2
Sequence 2, Application US/08458860A
Patent No. 6100390
GENERAL INFORMATION:
APPLICANT: Frank, Glenn R.
APPLICANT: Tripp, Cynthia A.
APPLICANT: Grievé, Robert B.
TITLE OF INVENTION: NOVEL PARASITIC HELMINTH
TITLE OF INVENTION: P22U NUCLEIC ACID MOLECULES
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESS: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver

```

```

STATE: CO
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,860A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-13-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/863-9700
TELEFAX: 303/863-0223
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-860A-2

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Query Match 4.1%; Score 146; DB 3; Length 303;
Best Local Similarity 24.6%; Pred. No. 1.6e-05;
Matches 52; Conservative 46; Mismatches 87; Indels 26; Gaps 10;

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```

QY 32 DROEYECRKQ--CMQLETS---GOMRRC--VSQCDKRFEE-----DIDMSKYDNDPP 78
DB 97 DDEDLDECSQGERPCRYLAKTLICVHLKICDGDGSDSDENKADDEVITISINNESI 156
QY 79 QTDCCQCCQRCRCQESGP--RQOQYCORR--CKEICEEBE--EYNRPDPQOQYEQCCQERC 133
DB 157 NTRCDQDQRC--ENGKICIAQIDRCNRKRYDCDDGTDETCFVQALQARGVTVDNA 213
QY 134 QRETEPRHMQTCQRCER-RYEKERKROOKRYEQQREDEEYERMKEDNKRPQOR 192
DB 214 IRDDELPTNTVSMEOKYDYQKEDKERRMOEEEOERLREYEOIQKLOEEREROEOE 273
QY 193 EYEDCRRCEOEPRQOYQCCQRCRCROQROH 223
DB 274 RKQKERERMEQERIRQEYD---EKERQROY 300

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RESULT 15
5210183-3
Patent No. 5210183
APPLICANT: LINDAHL, GUNNAR;FRITZ, ELISABET;HEDEN, LARS-OLOF
TITLE OF INVENTION: PROTEIN ARR, WITH IMMUNOGLOBULIN A
BINDING ACTIVITY, THE CORRESPONDING VECTORS AND HOSTS, REAGENT
AND PHARMACEUTICAL COMPOSITION
NUMBER OF SEQUENCES: 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/270,099
FILING DATE: 14-NOV-1988
PRIOR APPLICATION NUMBER: 186,097
APPLICATION NUMBER: 186,097
FILING DATE: 25-APR-1988
SEQ ID NO:3
LENGTH: 683
5210183-3

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Query Match 4.0%; Score 140.5; DB 5; Length 683;
Best Local Similarity 18.7%; Pred. No. 0.00018;
Matches 132; Conservative 128; Mismatches 236; Indels 209; Gaps 31;

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QY 79 QTDCCQCCQRCRCQESGP--PRQOYQCCQRCRCRCROQROH-----NRORDPQ----- 123

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```
Db 36 QTEVKAALIKPPQADSWAMNPKKEYNALLKENELKVEREKYLSYADDEKDPQYRALMGE 95
124 -----OQVEOCQERCOHETEPRIHMTQOORCERRY-----EKERKQOKRYEEOQREDEE 174
Db 96 NODLRKREGOYQDKIELELEKERKEKQEROQOLEROYOIEADKHQEOQKKHOEOQOLEA 155
175 KYERMKEE---DNKRDPQOREYEDCRR-----RCEQOEPRQOYOCORRCRE----- 218
Db 156 EKOKLADKQISDASRQGLSRDLEASRAKKELAEAOQKLEEKQOISDASRQGLSRDLEA 215
156 EKOKLADKQISDASRQGLSRDLEASRAKKELAEAOQKLEEKQOISDASRQGLSRDLEA 215
QY 219 -OQROHGRGDL-----INPQRGSGRYERDEKQSDNPPYFDEKSLSTRFT 265
Db 216 SRERKKKVEADLAANSKLOALEKLNKE-----LEEG-KKISEK-----EKAEIOARLEA 264
266 EEGHISYLENFYGRSKLLBALKNYRLVLEANPNAFLPT----- 305
Db 265 EAK--ALKEQOLAQAEELAKG-----NOTNAKVAPOANRSRSAMTQOKRTLPSTGE 316
306 ----HIDADAILLVYGGRCALMKIHRDNR-----ESYNLECGDYIRIPAGTTFY 350
Db 317 KANPFTAAATVWVSAGMLALKLKEENKKPOADSAMNPKKEYNALLKENELKVEREKY 376
351 LIRDNNEERLHAKETQISTPQOYKEFFPAGQONPEPYLSTFSKE----- 396
Db 377 LSYADKE-----KDPQYRALMGENODLRKREGOYQDK-IEELEKERKEKQEROQOLERQ 430
397 -ILEAALNTOAERLRGVLGOOREGVIISASQEOIRELTRDSESRMHIRGGESSRGPY 455
Db 431 YQIEADKHQEOQKK-----HOEOQOLEAEKQKQKLAQ-DKOISDASRQGLSRDLEASRA-- 483
456 NLENKRPLYSNKYGQAYEVKPEDYROLQDMQVSVFIANTITQSGMGPFFENTRSTKYVVA 515
Db 484 -----AKKELEAEHQKLEKEKQOISDAS-----RQGL-----SRDLEASREA 519
516 SGADYEMACPHLSGRH-----GGRRCGKRHEEEDVHYEQVAKRL-----SKRE 560
Db 520 KKKVEADLAA--LTAEHQKLEKEDKOISDASRQGLSRDLEASRERKKKVEADLAANSKLO 577
561 AIYVVPYGHVPVYSSGNENLLFAFGINAGNNIENFLAGRERNVLO--QIEPQAMELAF 617
Db 578 AL-----EKL-----NKELEGGKKLSEKKAELQARLEAEAKALKEOL 615
QY 618 AAPRKEVEELLFNSQDESIFEPGPR--OHQOOSRSTKQOQPLVS 659
618 AAPRKEVEELLFNSQDESIFEPGPR--OHQOOSRSTKQOQPLVS 659
Db 616 AKQAEELAKLKGNT-----PNAKVAPOANRSRSAMTQOKRTLP 655
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